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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Patent Application of

DAVIS, Peter D.

Atty. Ref.: 620-179

Serial No. 10/018,826

Group:

Filed: December 21, 2001

Examiner:

For: CHIMERIC PROTEINS MEDIATING TARGETED
APOPTOSIS

* * * * *

April 22, 2002

Assistant Commissioner for Patents
Washington, DC 20231

Sir:

STATEMENT

The attached paper and computer-readable copies of the Sequence Listing are the same. No new matter has been added.

Respectfully submitted,

NIXON & VANDERHYE P.C.

By: _____



B. J. Sadoff

Reg. No. 36,663

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SEQUENCE LISTING

<110> Davis, Peter D

<120> Chimeric proteins mediating targeted apoptosis

<130> 620-179

<140> US 10/018,826

<141> 2001-12-21

<150> PCT/GB00/02449

<151> 2000-06-26

<150> GB 9914650.8

<151> 1999-06-24

<160> 22

<170> PatentIn Ver. 2.1

<210> 1

<211> 84

<212> PRT

<213> Homo sapiens

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Gly Phe Val Arg Lys Asn Gly Val Asn Glu Ala Lys Ile Asp Glu Ile
20 25 30

Lys Asn Asp Asn Val Gln Asp Thr Ala Glu Gln Lys Val Gln Leu Leu
35 40 45

Arg Asn Trp His Gln Leu His Gly Lys Glu Ala Tyr Asp Thr Leu
50 55 60

Ile Lys Asp Leu Lys Ala Asn Leu Cys Thr Leu Ala Glu Lys Ile
65 70 75 80

Gln Thr Ile Ile

<210> 2

<211> 86

<212> PRT

<213> Homo sapiens

<400> 2

Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro Leu Arg Trp
1 5 10 15

Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu Ile Asp Arg
 20 25 30

Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln Tyr Ser Met
 35 40 45

Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr Leu Glu
 50 55 60

Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly Cys Leu Glu
 65 70 75 80

Asp Ile Glu Glu Ala Leu
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<210> 3
<211> 1468

<212> DNA

<213> Artificial Sequence

<220>
<221> CDS
<222> (116)..(1411)

<220>
<223> Description of Artificial Sequence: Nucleic acid
 construct encoding a chimeric protein containing
 the extracellular domain of CD44H and the
 transmembrane and cytoplasmic domains of human Fas

<400> 3
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cggccaggga tcctccagct cctttcgccc ggcgcctccg ttcgctccgg acacc atg 118
 Met
 1

gac aag ttt tgg tgg cac gca gcc tgg gga ctc tgc ctc gtg ccg ctg 166
 Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro Leu
 5 10 15

agc ctg gcg cag atc gat ttg aat ata acc tgc cgc ttt gca ggt gta 214
 Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly Val
 20 25 30

ttc cac gtg gag aaa aat ggt cgc tac agc atc tct cgg acg gag gcc 262
 Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu Ala
 35 40 45

gct gac ctc tgc aag gct ttc aat agc acc ttg ccc aca atg gcc cag 310
 Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala Gln
 50 55 60 65

atg gag aaa gct ctg agc atc gga ttt gag acc tgc agg tat ggg ttc 358
 Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly Phe
 70 75 80

ata gaa ggg cat gtg gtg att ccc cgg atc cac ccc aac tcc atc tgt Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile Cys 85 90 95	406
gca gca aac aac aca ggg gtg tac atc ctc aca tac aac acc tcc cag Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser Gln 100 105 110	454
tat gac aca tat tgc ttc aat gct tca gct cca cct gaa gaa gat tgt Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp Cys 115 120 125	502
aca tca gtc aca gac ctg ccc aat gcc ttt gat gga cca att acc ata Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr Ile 130 135 140 145	550
act att gtt aac cgt gat ggc acc cgc tat gtc cag aaa gga gaa tac Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu Tyr 150 155 160	598
aga acg aat cct gaa gac atc tac ccc agc aac cct act gat gat gac Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp Asp 165 170 175	646
gtg agc agc ggc tcc tcc agt gaa agg agc agc act tca gga ggt tac Val Ser Ser Gly Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly Tyr 180 185 190	694
atc ttt tac acc ttt tct act gta cac ccc atc cca gac gaa gac agt Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp Ser 195 200 205	742
ccc tgg atc acc gac agc aca gac aga atc cct gct acc aga gac caa Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Ala Thr Arg Asp Gln 210 215 220 225	790
gac aca ttc cac ccc agt ggg ggg tcc cat acc act cat gga tct gaa Asp Thr Phe His Pro Ser Gly Ser His Thr Thr His Gly Ser Glu 230 235 240	838
tca gat gga cac tca cat ggg agt caa gaa ggt gga gca aac aca acc Ser Asp Gly His Ser His Gly Ser Gln Glu Gly Ala Asn Thr Thr 245 250 255	886
tct ggt cct ata agg aca ccc caa att cca gaa tgg ctg atc atc ctt Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp Leu Ile Ile Leu 260 265 270	934
tgt ctt ctt ctt ttg cca att cca cta att gtt tgg gtg aag aga aag Cys Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg Lys 275 280 285	982
gaa gta cag aaa aca tgc aga aag cac aga aag gaa aac caa ggt tct Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly Ser 290 295 300 305	1030

cat gaa tct cca acc tta aat cct gaa aca gtg gca ata aat tta tct		1078	
His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val Ala Ile Asn Leu Ser			
310	315	320	
gat gtt gac ttg agt aaa tat atc acc act att gct gga gtc atg aca		1126	
Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Ile Ala Gly Val Met Thr			
325	330	335	
cta agt caa gtt aaa ggc ttt gtt cga aag aat ggt gtc aat gaa gcc		1174	
Leu Ser Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu Ala			
340	345	350	
aaa ata gat gag atc aag aat gac aat gtc caa gac aca gaa cag		1222	
Lys Ile Asp Glu Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu Gln			
355	360	365	
aaa gtt caa ctg ctt cgt aat tgg cat caa ctt cat gga aag aaa gaa		1270	
Lys Val Gln Leu Leu Arg Asn Trp His Gln Leu His Gly Lys Lys Glu			
370	375	380	385
gcg tat gac aca ttg att aaa gat ctc aaa aaa gcc aat ctt tgt act		1318	
Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys Thr			
390	395	400	
ctt gca ggg aaa att cag act atc atc ctc aag gac att act agt gac		1366	
Leu Ala Gly Lys Ile Gln Thr Ile Ile Leu Lys Asp Ile Thr Ser Asp			
405	410	415	
tca gaa aat tca aac ttc aga aat gaa atc caa agc ttg gtc tag		1411	
Ser Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln Ser Leu Val			
420	425	430	
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<210> 4

<211> 431

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chimeric protein containing the extracellular domain of CD44H and the transmembrane and cytoplasmic domains of human Fas

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20	25	30	
Val Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu			
35	40	45	
Ala Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala			
50	55	60	
Gln Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly			
65	70	75	80

Phe	Ile	Glu	Gly	His	Val	Val	Ile	Pro	Arg	Ile	His	Pro	Asn	Ser	Ile
					85				90						95
Cys	Ala	Ala	Asn	Asn	Thr	Gly	Val	Tyr	Ile	Leu	Thr	Tyr	Asn	Thr	Ser
					100				105						110
Gln	Tyr	Asp	Thr	Tyr	Cys	Phe	Asn	Ala	Ser	Ala	Pro	Pro	Glu	Glu	Asp
					115				120						125
Cys	Thr	Ser	Val	Thr	Asp	Leu	Pro	Asn	Ala	Phe	Asp	Gly	Pro	Ile	Thr
					130				135						140
Ile	Thr	Ile	Val	Asn	Arg	Asp	Gly	Thr	Arg	Tyr	Val	Gln	Lys	Gly	Glu
					145				150						160
Tyr	Arg	Thr	Asn	Pro	Glu	Asp	Ile	Tyr	Pro	Ser	Asn	Pro	Thr	Asp	Asp
					165				170						175
Asp	Val	Ser	Ser	Gly	Ser	Ser	Ser	Glu	Arg	Ser	Ser	Thr	Ser	Gly	Gly
					180				185						190
Tyr	Ile	Phe	Tyr	Thr	Phe	Ser	Thr	Val	His	Pro	Ile	Pro	Asp	Glu	Asp
					195				200						205
Ser	Pro	Trp	Ile	Thr	Asp	Ser	Thr	Asp	Arg	Ile	Pro	Ala	Thr	Arg	Asp
					210				215						220
Gln	Asp	Thr	Phe	His	Pro	Ser	Gly	Gly	Ser	His	Thr	Thr	His	Gly	Ser
					225				230						240
Glu	Ser	Asp	Gly	His	Ser	His	Gly	Ser	Gln	Glu	Gly	Gly	Ala	Asn	Thr
					245				250						255
Thr	Ser	Gly	Pro	Ile	Arg	Thr	Pro	Gln	Ile	Pro	Glu	Trp	Leu	Ile	Ile
					260				265						270
Leu	Cys	Leu	Leu	Leu	Leu	Pro	Ile	Pro	Leu	Ile	Val	Trp	Val	Lys	Arg
					275				280						285
Lys	Glu	Val	Gln	Lys	Thr	Cys	Arg	Lys	His	Arg	Lys	Glu	Asn	Gln	Gly
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Ser	His	Glu	Ser	Pro	Thr	Leu	Asn	Pro	Glu	Thr	Val	Ala	Ile	Asn	Leu
					305				310						320
Ser	Asp	Val	Asp	Leu	Ser	Lys	Tyr	Ile	Thr	Thr	Ile	Ala	Gly	Val	Met
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Thr	Leu	Ser	Gln	Val	Lys	Gly	Phe	Val	Arg	Lys	Asn	Gly	Val	Asn	Glu
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Ala	Lys	Ile	Asp	Glu	Ile	Lys	Asn	Asp	Asn	Val	Gln	Asp	Thr	Ala	Glu
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Gln	Lys	Val	Gln	Leu	Leu	Arg	Asn	Trp	His	Gln	Leu	His	Gly	Lys	Lys
					370				375						380
Glu	Ala	Tyr	Asp	Thr	Leu	Ile	Lys	Asp	Leu	Lys	Lys	Ala	Asn	Leu	Cys
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Thr	Leu	Ala	Gly	Lys	Ile	Gln	Thr	Ile	Ile	Leu	Lys	Asp	Ile	Thr	Ser
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Asp	Ser	Glu	Asn	Ser	Asn	Phe	Arg	Asn	Glu	Ile	Gln	Ser	Leu	Val	
					420				425						430

act att gtt aac cgt gat ggc acc cgc tat gtc cag aaa gga gaa tac Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu Tyr 150 155 160	598
aga acg aat cct gaa gac atc tac ccc agc aac cct act gat gat gac Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp Asp 165 170 175	646
gtg agc agc ggc tcc tcc agt gaa agg agc agc act tca gga ggt tac Val Ser Ser Gly Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly Tyr 180 185 190	694
atc ttt tac acc ttt tct act gta cac ccc atc cca gac gaa gac agt Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp Ser 195 200 205	742
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gac aca ttc cac ccc agt ggg ggg tcc cat acc act cat gga tct gaa Asp Thr Phe His Pro Ser Gly Gly Ser His Thr Thr His Gly Ser Glu 230 235 240	838
tca gat gga cac tca cat ggg agt caa gaa ggt gga gca aac aca acc Ser Asp Gly His Ser His Gly Ser Gln Glu Gly Gly Ala Asn Thr Thr 245 250 255	886
tct ggt cct ata agg aca ccc caa att cca gaa tgg ctg atc atc ttg Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp Leu Ile Ile Leu 260 265 270	934
gca tcc ctc ttg gcc ttg gct ttg att ctt gca gtt tgc att gca gtc Ala Ser Leu Ala Leu Ala Leu Ile Leu Ala Val Cys Ile Ala Val 275 280 285	982
ggg gtg aag aga aag gaa gta cag aaa aca tgc aga aag cac aga aag Gly Val Lys Arg Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys 290 295 300 305	1030
gaa aac caa ggt tct cat gaa tct cca acc tta aat cct gaa aca gtg Glu Asn Gln Gly Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val 310 315 320	1078
gca ata aat tta tct gat gtt gac ttg agt aaa tat atc acc act att Ala Ile Asn Leu Ser Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Ile 325 330 335	1126
gct gga gtc atg aca cta agt caa gtt aaa ggc ttt gtt cga aag aat Ala Gly Val Met Thr Leu Ser Gln Val Lys Gly Phe Val Arg Lys Asn 340 345 350	1174
ggt gtc aat gaa gcc aaa ata gat gag atc aag aat gac aat gtc caa Gly Val Asn Glu Ala Lys Ile Asp Glu Ile Lys Asn Asp Asn Val Gln 355 360 365	1222

gac aca gca gaa cag aaa gtt caa ctg ctt cgt aat tgg cat caa ctt	1270
Asp Thr Ala Glu Gln Lys Val Gln Leu Leu Arg Asn Trp His Gln Leu	
370 375 380 385	
cat gga aag aaa gaa gcg tat gac aca ttg att aaa gat ctc aaa aaa	1318
His Gly Lys Lys Glu Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys Lys	
390 395 400	
gcc aat ctt tgt act ctt gca ggg aaa att cag act atc atc ctc aag	1366
Ala Asn Leu Cys Thr Leu Ala Gly Lys Ile Gln Thr Ile Ile Leu Lys	
405 410 415	
gac att act agt gac tca gaa aat tca aac ttc aga aat gaa atc caa	1414
Asp Ile Thr Ser Asp Ser Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln	
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<211> 436

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chimeric protein containing the extracellular and transmembrane domains of CD44H and the cytoplasmic domain of human Fas

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20 25 30	
Val Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu	
35 40 45	
Ala Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala	
50 55 60	
Gln Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly	
65 70 75 80	
Phe Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile	
85 90 95	
Cys Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser	
100 105 110	
Gln Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp	
115 120 125	
Cys Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr	
130 135 140	
Ile Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu	
145 150 155 160	
Tyr Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp	
165 170 175	

Asp Val Ser Ser Gly Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly
 180 185 190
 Tyr Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp
 195 200 205
 Ser Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Ala Thr Arg Asp
 210 215 220
 Gln Asp Thr Phe His Pro Ser Gly Gly Ser His Thr Thr His Gly Ser
 225 230 235 240
 Glu Ser Asp Gly His Ser His Gly Ser Gln Glu Gly Gly Ala Asn Thr
 245 250 255
 Thr Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp Leu Ile Ile
 260 265 270
 Leu Ala Ser Leu Ala Leu Ala Leu Ile Leu Ala Val Cys Ile Ala
 275 280 285
 Val Gly Val Lys Arg Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg
 290 295 300
 Lys Glu Asn Gln Gly Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr
 305 310 315 320
 Val Ala Ile Asn Leu Ser Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr
 325 330 335
 Ile Ala Gly Val Met Thr Leu Ser Gln Val Lys Gly Phe Val Arg Lys
 340 345 350
 Asn Gly Val Asn Glu Ala Lys Ile Asp Glu Ile Lys Asn Asp Asn Val
 355 360 365
 Gln Asp Thr Ala Glu Gln Lys Val Gln Leu Leu Arg Asn Trp His Gln
 370 375 380
 Leu His Gly Lys Lys Glu Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys
 385 390 395 400
 Lys Ala Asn Leu Cys Thr Leu Ala Gly Lys Ile Gln Thr Ile Ile Leu
 405 410 415
 Lys Asp Ile Thr Ser Asp Ser Glu Asn Ser Asn Phe Arg Asn Glu Ile
 420 425 430
 Gln Ser Leu Val
 435

<210> 7
 <211> 3009
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (190)..(2952)

<220>
 <223> Description of Artificial Sequence: Nucleic acid construct
 encoding chimeric protein containing the extracellular
 domain of Flt-1 fused in-frame to the transmembrane and
 cytoplasmic domains of Fas

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gactctggcg gccgggtcgt tggccggggg agcgcggca cggggcgagc aggccgcgtc 180
 gcgctcacc atg gtc agc tac tgg gac acc ggg gtc ctg ctg tgc gcg ctg 231
 Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu
 1 5 10

 ctc agc tgt ctg ctt ctc aca gga tct agt tca ggt tca aaa tta aaa 279
 Leu Ser Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys
 15 20 25 30

 gat cct gaa ctg agt tta aaa ggc acc cag cac atc atg caa gca ggc 327
 Asp Pro Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly
 35 40 45

 cag aca ctg cat ctc caa tgc agg ggg gaa gca gcc cat aaa tgg tct 375
 Gln Thr Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser
 50 55 60

 ttg cct gaa atg gtg agt aag gaa agc gaa agg ctg agc ata act aaa 423
 Leu Pro Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys
 65 70 75

 tct gcc tgt gga aga aat ggc aaa caa ttc tgc agt act tta acc ttg 471
 Ser Ala Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu
 80 85 90

 aac aca gct caa gca aac cac act ggc ttc tac agc tgc aaa tat cta 519
 Asn Thr Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu
 95 100 105 110

 gct gta cct act tca aag aag gaa aca gaa tct gca atc tat ata 567
 Ala Val Pro Thr Ser Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile
 115 120 125

 ttt att agt gat aca ggt aga cct ttc gta gag atg tac agt gaa atc 615
 Phe Ile Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile
 130 135 140

 ccc gaa att ata cac atg act gaa gga agg gag ctc gtc att ccc tgc 663
 Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys
 145 150 155

 cggtt acg tca cct aac atc act gtt act tta aaa aag ttt cca ctt 711
 Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu
 160 165 170

 gac act ttg atc cct gat gga aaa cgc ata atc tgg gac agt aga aag 759
 Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys
 175 180 185 190

 ggc ttc atc ata tca aat gca acg tac aaa gaa ata ggg ctt ctg acc 807
 Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr
 195 200 205

 tgt gaa gca aca gtc aat ggg cat ttg tat aag aca aac tat ctc aca 855
 Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr
 210 215 220

cat cga caa acc aat aca atc ata gat gtc caa ata agc aca cca cgc His Arg Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg 225 230 235	903
cca gtc aaa tta ctt aga ggc cat act ctt gtc ctc aat tgt act gct Pro Val Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala 240 245 250	951
acc act ccc ttg aac acg aga gtt caa atg acc tgg agt tac cct gat Thr Thr Pro Leu Asn Thr Arg Val Gln Met Thr Trp Ser Tyr Pro Asp 255 260 265 270	999
gaa aaa aat aag aga gct tcc gta agg cga cga att gac caa agc aat Glu Lys Asn Lys Arg Ala Ser Val Arg Arg Arg Ile Asp Gln Ser Asn 275 280 285	1047
tcc cat gcc aac ata ttc tac agt gtt ctt act att gac aaa atg cag Ser His Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln 290 295 300	1095
aac aaa gac aaa gga ctt tat act tgt cgt gta agg agt gga cca tca Asn Lys Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser 305 310 315	1143
ttc aaa tct gtt aac acc tca gtg cat ata tat gat aaa gca ttc atc Phe Lys Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Phe Ile 320 325 330	1191
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gtt gta tgg tta aaa gat ggg tta cct gcg act gag aaa tct gct cgc Val Val Trp Leu Lys Asp Gly Leu Pro Ala Thr Glu Lys Ser Ala Arg 370 375 380	1335
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gat gca ggg aat tat aca atc ttg ctg agc ata aaa cag tca aat gtg Asp Ala Gly Asn Tyr Thr Ile Leu Leu Ser Ile Lys Gln Ser Asn Val 400 405 410	1431
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aca atc aag tgg ttc tgg cac ccc tgt aac cat aat cat tcc gaa gca Thr Ile Lys Trp Phe Trp His Pro Cys Asn His Asn His Ser Glu Ala 465 470 475	1623
agg tgt gac ttt tgt tcc aat aat gaa gag tcc ttt atc ctg gat gct Arg Cys Asp Phe Cys Ser Asn Asn Glu Glu Ser Phe Ile Leu Asp Ala 480 485 490	1671
gac agc aac atg gga aac aga att gag agc atc act cag cgc atg gca Asp Ser Asn Met Gly Asn Arg Ile Glu Ser Ile Thr Gln Arg Met Ala 495 500 505 510	1719
ata ata gaa gga aag aat aag atg gct agc acc ttg gtt gtg gct gac Ile Ile Glu Gly Lys Asn Lys Met Ala Ser Thr Leu Val Val Ala Asp 515 520 525	1767
tct aga att tct gga atc tac att tgc ata gct tcc aat aaa gtt ggg Ser Arg Ile Ser Gly Ile Tyr Ile Cys Ile Ala Ser Asn Lys Val Gly 530 535 540	1815
act gtg gga aga aac ata agc ttt tat atc aca gat gtg cca aat ggg Thr Val Gly Arg Asn Ile Ser Phe Tyr Ile Thr Asp Val Pro Asn Gly 545 550 555	1863
ttt cat gtt aac ttg gaa aaa atg ccg acg gaa gga gag gac ctg aaa Phe His Val Asn Leu Glu Lys Met Pro Thr Glu Gly Glu Asp Leu Lys 560 565 570	1911
ctg tct tgc aca gtt aac aag ttc tta tac aga gac gtt act tgg att Leu Ser Cys Thr Val Asn Lys Phe Leu Tyr Arg Asp Val Thr Trp Ile 575 580 585 590	1959
tta ctg cgg aca gtt aat aac aga aca atg cac tac agt att agc aag Leu Leu Arg Thr Val Asn Asn Arg Thr Met His Tyr Ser Ile Ser Lys 595 600 605	2007
caa aaa atg gcc atc act aag gag cac tcc atc act ctt aat ctt acc Gln Lys Met Ala Ile Thr Lys Glu His Ser Ile Thr Leu Asn Leu Thr 610 615 620	2055
atc atg aat gtt tcc ctg caa gat tca ggc acc tat gcc tgc aga gcc Ile Met Asn Val Ser Leu Gln Asp Ser Gly Thr Tyr Ala Cys Arg Ala 625 630 635	2103
agg aat gta tac aca ggg gaa gaa atc ctc cag aag aaa gaa att aca Arg Asn Val Tyr Thr Gly Glu Glu Ile Leu Gln Lys Lys Glu Ile Thr 640 645 650	2151
atc aga gat cag gaa gca cca tac ctc ctg cga aac ctc agt gat cac Ile Arg Asp Gln Glu Ala Pro Tyr Leu Leu Arg Asn Leu Ser Asp His 655 660 665 670	2199

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gtc ccc gag cct cag atc act tgg ttt aaa aac aac cac aaa ata caa Val Pro Glu Pro Gln Ile Thr Trp Phe Lys Asn Asn His Lys Ile Gln 690 695 700	2295
caa gag cct gga att att tta gga cca gga agc agc acg ctg ttt att Gln Glu Pro Gly Ile Ile Leu Gly Pro Gly Ser Ser Thr Leu Phe Ile 705 710 715	2343
gaa aga gtc aca gaa gag gat gaa ggt gtc tat cac tgc aaa gcc acc Glu Arg Val Thr Glu Glu Asp Glu Gly Val Tyr His Cys Lys Ala Thr 720 725 730	2391
aac cag aag ggc tct gtg gaa agt tca gca tac ctc act gtt caa gga Asn Gln Lys Gly Ser Val Glu Ser Ser Ala Tyr Leu Thr Val Gln Gly 735 740 745 750	2439
acc tcg gac gga tcc aga tct aac ttg ggg tgg ctt tgt ctt ctt ctt Thr Ser Asp Gly Ser Arg Ser Asn Leu Gly Trp Leu Cys Leu Leu 755 760 765	2487
ttg cca att cca cta att gtt tgg gtg aag aga aag gaa gta cag aaa Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg Lys Glu Val Gln Lys 770 775 780	2535
aca tgc aga aag cac aga aag gaa aac caa ggt tct cat gaa tct cca Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly Ser His Glu Ser Pro 785 790 795	2583
acc tta aat cct gaa aca gtg gca ata aat tta tct gat gtt gac ttg Thr Leu Asn Pro Glu Thr Val Ala Ile Asn Leu Ser Asp Val Asp Leu 800 805 810	2631
agt aaa tat atc acc act att gct gga gtc atg aca cta agt caa gtt Ser Lys Tyr Ile Thr Thr Ile Ala Gly Val Met Thr Leu Ser Gln Val 815 820 825 830	2679
aaa ggc ttt gtt cga aag aat ggt gtc aat gaa gcc aaa ata gat gag Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu Ala Lys Ile Asp Glu 835 840 845	2727
atc aag aat gac aat gtc caa gac aca gca gaa cag aaa gtt caa ctg Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu Gln Lys Val Gln Leu 850 855 860	2775
ctt cgt aat tgg cat caa ctt cat gga aag aaa gaa gcg tat gac aca Leu Arg Asn Trp His Gln Leu His Gly Lys Lys Glu Ala Tyr Asp Thr 865 870 875	2823
ttg att aaa gat ctc aaa aaa gcc aat ctt tgt act ctt gca ggg aaa Leu Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys Thr Leu Ala Gly Lys 880 885 890	2871

att cag act atc atc ctc aag gac att act agt gac tca gaa aat tca 2919
Ile Gln Thr Ile Ile Leu Lys Asp Ile Thr Ser Asp Ser Glu Asn Ser
895 900 905 910

aac ttc aga aat gaa atc caa agc ttg gtc tag agtggaaaac aacaaattca 2972
Asn Phe Arg Asn Glu Ile Gln Ser Leu Val
915 920

gttctgagta tatgcaatta gtgtttaaaa agattct 3009

<210> 8
<211> 920
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chimeric protein containing the extracellular domain of Flt-1 fused in-frame to the transmembrane and cytoplasmic domains of Fas

<400> 8

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Cys	Leu	Leu	Leu	Thr	Gly	Ser	Ser	Ser	Gly	Ser	Lys	Leu	Lys	Asp	Pro
				20					25					30	
Glu	Leu	Ser	Leu	Lys	Gly	Thr	Gln	His	Ile	Met	Gln	Ala	Gly	Gln	Thr
				35					40					45	
Leu	His	Leu	Gln	Cys	Arg	Gly	Glu	Ala	Ala	His	Lys	Trp	Ser	Leu	Pro
				50			55				60				
Glu	Met	Val	Ser	Lys	Glu	Ser	Glu	Arg	Leu	Ser	Ile	Thr	Lys	Ser	Ala
				65			70				75				80
Cys	Gly	Arg	Asn	Gly	Lys	Gln	Phe	Cys	Ser	Thr	Leu	Thr	Leu	Asn	Thr
				85					90					95	
Ala	Gln	Ala	Asn	His	Thr	Gly	Phe	Tyr	Ser	Cys	Lys	Tyr	Leu	Ala	Val
				100				105						110	
Pro	Thr	Ser	Lys	Lys	Lys	Glu	Thr	Glu	Ser	Ala	Ile	Tyr	Ile	Phe	Ile
				115				120						125	
Ser	Asp	Thr	Gly	Arg	Pro	Phe	Val	Glu	Met	Tyr	Ser	Glu	Ile	Pro	Glu
				130			135							140	
Ile	Ile	His	Met	Thr	Glu	Gly	Arg	Glu	Leu	Val	Ile	Pro	Cys	Arg	Val
				145			150				155				160
Thr	Ser	Pro	Asn	Ile	Thr	Val	Thr	Leu	Lys	Lys	Phe	Pro	Leu	Asp	Thr
					165				170					175	
Leu	Ile	Pro	Asp	Gly	Lys	Arg	Ile	Ile	Trp	Asp	Ser	Arg	Lys	Gly	Phe
				180				185						190	
Ile	Ile	Ser	Asn	Ala	Thr	Tyr	Lys	Glu	Ile	Gly	Leu	Leu	Thr	Cys	Glu
				195				200						205	
Ala	Thr	Val	Asn	Gly	His	Leu	Tyr	Lys	Thr	Asn	Tyr	Leu	Thr	His	Arg
				210			215							220	
Gln	Thr	Asn	Thr	Ile	Ile	Asp	Val	Gln	Ile	Ser	Thr	Pro	Arg	Pro	Val
				225			230				235				240
Lys	Leu	Leu	Arg	Gly	His	Thr	Leu	Val	Leu	Asn	Cys	Thr	Ala	Thr	Thr
					245				250					255	
Pro	Leu	Asn	Thr	Arg	Val	Gln	Met	Thr	Trp	Ser	Tyr	Pro	Asp	Glu	Lys
				260				265						270	

Asn Lys Arg Ala Ser Val Arg Arg Arg Ile Asp Gln Ser Asn Ser His
 275 280 285
 Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys
 290 295 300
 Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys
 305 310 315 320
 Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Phe Ile Thr Val
 325 330 335
 Lys His Arg Lys Gln Gln Val Leu Glu Thr Val Ala Gly Lys Arg Ser
 340 345 350
 Tyr Arg Leu Ser Met Lys Val Lys Ala Phe Pro Ser Pro Glu Val Val
 355 360 365
 Trp Leu Lys Asp Gly Leu Pro Ala Thr Glu Lys Ser Ala Arg Tyr Leu
 370 375 380
 Thr Arg Gly Tyr Ser Leu Ile Ile Lys Asp Val Thr Glu Glu Asp Ala
 385 390 395 400
 Gly Asn Tyr Thr Ile Leu Leu Ser Ile Lys Gln Ser Asn Val Phe Lys
 405 410 415
 Asn Leu Thr Ala Thr Leu Ile Val Asn Val Lys Pro Gln Ile Tyr Glu
 420 425 430
 Lys Ala Val Ser Ser Phe Pro Asp Pro Ala Leu Tyr Pro Leu Gly Ser
 435 440 445
 Arg Gln Ile Leu Thr Cys Thr Ala Tyr Gly Ile Pro Gln Pro Thr Ile
 450 455 460
 Lys Trp Phe Trp His Pro Cys Asn His Asn His Ser Glu Ala Arg Cys
 465 470 475 480
 Asp Phe Cys Ser Asn Asn Glu Glu Ser Phe Ile Leu Asp Ala Asp Ser
 485 490 495
 Asn Met Gly Asn Arg Ile Glu Ser Ile Thr Gln Arg Met Ala Ile Ile
 500 505 510
 Glu Gly Lys Asn Lys Met Ala Ser Thr Leu Val Val Ala Asp Ser Arg
 515 520 525
 Ile Ser Gly Ile Tyr Ile Cys Ile Ala Ser Asn Lys Val Gly Thr Val
 530 535 540
 Gly Arg Asn Ile Ser Phe Tyr Ile Thr Asp Val Pro Asn Gly Phe His
 545 550 555 560
 Val Asn Leu Glu Lys Met Pro Thr Glu Gly Glu Asp Leu Lys Leu Ser
 565 570 575
 Cys Thr Val Asn Lys Phe Leu Tyr Arg Asp Val Thr Trp Ile Leu Leu
 580 585 590
 Arg Thr Val Asn Asn Arg Thr Met His Tyr Ser Ile Ser Lys Gln Lys
 595 600 605
 Met Ala Ile Thr Lys Glu His Ser Ile Thr Leu Asn Leu Thr Ile Met
 610 615 620
 Asn Val Ser Leu Gln Asp Ser Gly Thr Tyr Ala Cys Arg Ala Arg Asn
 625 630 635 640
 Val Tyr Thr Gly Glu Glu Ile Leu Gln Lys Lys Glu Ile Thr Ile Arg
 645 650 655
 Asp Gln Glu Ala Pro Tyr Leu Leu Arg Asn Leu Ser Asp His Thr Val
 660 665 670
 Ala Ile Ser Ser Ser Thr Thr Leu Asp Cys His Ala Asn Gly Val Pro
 675 680 685
 Glu Pro Gln Ile Thr Trp Phe Lys Asn Asn His Lys Ile Gln Gln Glu
 690 695 700
 Pro Gly Ile Ile Leu Gly Pro Gly Ser Ser Thr Leu Phe Ile Glu Arg
 705 710 715 720

Val	Thr	Glu	Glu	Asp	Glu	Gly	Val	Tyr	His	Cys	Lys	Ala	Thr	Asn	Gln
							725		730						735
Lys	Gly	Ser	Val	Glu	Ser	Ser	Ala	Tyr	Leu	Thr	Val	Gln	Gly	Thr	Ser
							740		745						750
Asp	Gly	Ser	Arg	Ser	Asn	Leu	Gly	Trp	Leu	Cys	Leu	Leu	Leu	Leu	Pro
							755		760						765
Ile	Pro	Leu	Ile	Val	Trp	Val	Lys	Arg	Lys	Glu	Val	Gln	Lys	Thr	Cys
							770		775						780
Arg	Lys	His	Arg	Lys	Glu	Asn	Gln	Gly	Ser	His	Glu	Ser	Pro	Thr	Leu
							785		790						800
Asn	Pro	Glu	Thr	Val	Ala	Ile	Asn	Leu	Ser	Asp	Val	Asp	Leu	Ser	Lys
							805		810						815
Tyr	Ile	Thr	Thr	Ile	Ala	Gly	Val	Met	Thr	Leu	Ser	Gln	Val	Lys	Gly
							820		825						830
Phe	Val	Arg	Lys	Asn	Gly	Val	Asn	Glu	Ala	Lys	Ile	Asp	Glu	Ile	Lys
							835		840						845
Asn	Asp	Asn	Val	Gln	Asp	Thr	Ala	Glu	Gln	Lys	Val	Gln	Leu	Leu	Arg
							850		855						860
Asn	Trp	His	Gln	Leu	His	Gly	Lys	Lys	Glu	Ala	Tyr	Asp	Thr	Leu	Ile
							865		870						880
Lys	Asp	Leu	Lys	Lys	Ala	Asn	Leu	Cys	Thr	Leu	Ala	Gly	Lys	Ile	Gln
							885		890						895
Thr	Ile	Ile	Leu	Lys	Asp	Ile	Thr	Ser	Asp	Ser	Glu	Asn	Ser	Asn	Phe
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Arg	Asn	Glu	Ile	Gln	Ser	Leu	Val								
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<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (169) .. (2952)

<220>
<223> Description of Artificial Sequence: Nucleic acid construct
encoding chimeric protein containing the extracellular
domain of Flk-1 fused in-frame to the transmembrane and
cytoplasmic domains of Fas

```

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Lys Val Leu Leu Ala Val Ala Leu Trp Leu Cys Val Glu Thr Arg Ala

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gcc tct gtg ggt ttg cct agt gtt tct ctt gat ctg ccc agg ctc agc Ala Ser Val Gly Leu Pro Ser Val Ser Leu Asp Leu Pro Arg Leu Ser 20 25 30 35	273
ata caa aaa gac ata ctt aca att aag gct aat aca act ctt caa att Ile Gln Lys Asp Ile Leu Thr Ile Lys Ala Asn Thr Thr Leu Gln Ile 40 45 50	321
act tgc agg gga cag agg gac ttg gac tgg ctt tgg ccc aat aat cag Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro Asn Asn Gln 55 60 65	369
agt ggc agt gag caa agg gtg gag gtg act gag tgc agc gat ggc ctc Ser Gly Ser Glu Gln Arg Val Glu Val Thr Glu Cys Ser Asp Gly Leu 70 75 80	417
ttc tgt aag aca ctc aca att cca aaa gtg atc gga aat gac act gga Phe Cys Lys Thr Leu Thr Ile Pro Lys Val Ile Gly Asn Asp Thr Gly 85 90 95	465
gcc tac aag tgc ttc tac cgg gaa act gac ttg gcc tcg gtc att tat Ala Tyr Lys Cys Phe Tyr Arg Glu Thr Asp Leu Ala Ser Val Ile Tyr 100 105 110 115	513
gtc tat gtt caa gat tac aga tct cca ttt att gct tct gtt agt gac Val Tyr Val Gln Asp Tyr Arg Ser Pro Phe Ile Ala Ser Val Ser Asp 120 125 130	561
caa cat gga gtc gtg tac att act gag aac aaa aac aaa act gtg gtg Gln His Gly Val Val Tyr Ile Thr Glu Asn Lys Asn Lys Thr Val Val 135 140 145	609
att cca tgt ctc ggg tcc att tca aat ctc aac gtg tca ctt tgt gca Ile Pro Cys Leu Gly Ser Ile Ser Asn Leu Asn Val Ser Leu Cys Ala 150 155 160	657
aga tac cca gaa aag aga ttt gtt cct gat ggt aac aga att tcc tgg Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg Ile Ser Trp 165 170 175	705
gac agc aag aag ggc ttt act att ccc agc tac atg atc agc tat gct Asp Ser Lys Lys Gly Phe Thr Ile Pro Ser Tyr Met Ile Ser Tyr Ala 180 185 190 195	753
ggc atg gtc ttc tgt gaa gca aaa att aat gat gaa agt tac cag tct Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp Glu Ser Tyr Gln Ser 200 205 210	801
att atg tac ata gtt gtc gtt gta ggg tat agg att tat gat gtg gtt Ile Met Tyr Ile Val Val Val Gly Tyr Arg Ile Tyr Asp Val Val 215 220 225	849
ctg agt ccg tct cat gga att gaa cta tct gtt gga gaa aag ctt gtc Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu Lys Leu Val 230 235 240	897

tta aat tgt aca gca aga act gaa cta aat gtg ggg att gac ttc aac Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile Asp Phe Asn 245 250 255	945
tgg gaa tac cct tct tcg aag cat cag cat aag aaa ctt gta aac cga Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu Val Asn Arg 260 265 270 275	993
gac cta aaa acc cag tct ggg agt gag atg aag aaa ttt ttg agc acc Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe Leu Ser Thr 280 285 290	1041
tta act ata gat ggt gta acc cgg agt gac caa gga ttg tac acc tgt Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu Tyr Thr Cys 295 300 305	1089
gca gca tcc agt ggg ctg atg acc aag aag aac agc aca ttt gtc agg Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr Phe Val Arg 310 315 320	1137
gtc cat gaa aaa cct ttt gtt gct ttt gga agt ggc atg gaa tct ctg Val His Glu Lys Pro Phe Val Ala Phe Gly Ser Gly Met Glu Ser Leu 325 330 335	1185
gtg gaa gcc acg gtg ggg gag cgt gtc aga atc cct gcg aag tac ctt Val Glu Ala Thr Val Gly Glu Arg Val Arg Ile Pro Ala Lys Tyr Leu 340 345 350 355	1233
gtt tac cca ccc cca gaa ata aaa tgg tat aaa aat gga ata ccc ctt Gly Tyr Pro Pro Glu Ile Lys Trp Tyr Lys Asn Gly Ile Pro Leu 360 365 370	1281
gag tcc aat cac aca att aaa gcg ggg cat gta ctg acg att atg gaa Glu Ser Asn His Thr Ile Lys Ala Gly His Val Leu Thr Ile Met Glu 375 380 385	1329
gtg agt gaa aga gac aca gga aat tac act gtc atc ctt acc aat ccc Val Ser Glu Arg Asp Thr Gly Asn Tyr Thr Val Ile Leu Thr Asn Pro 390 395 400	1377
att tca aag gag aag cag agc cat gtg gtc tct ctg gtt gtg tat gtc Ile Ser Lys Glu Lys Gln Ser His Val Val Ser Leu Val Val Tyr Val 405 410 415	1425
cca ccc cag att ggt gag aaa tct cta atc tct cct gtg gat tcc tac Pro Pro Gln Ile Gly Glu Lys Ser Leu Ile Ser Pro Val Asp Ser Tyr 420 425 430 435	1473
cag tac ggc acc actcaa acg ctg aca tgt acg gtc tat gcc att cct Gln Tyr Gly Thr Thr Gln Thr Leu Thr Cys Thr Val Tyr Ala Ile Pro 440 445 450	1521
ccc ccg cat cac atc cac tgg tat tgg cag ttg gag gaa gag tgc gcc Pro Pro His His Ile His Trp Tyr Trp Gln Leu Glu Glu Cys Ala 455 460 465	1569

aac gag ccc agc caa gct gtc tca gtg aca aac cca tac cct tgt gaa Asn Glu Pro Ser Gln Ala Val Ser Val Thr Asn Pro Tyr Pro Cys Glu 470	475	480	1617
gaa tgg aga agt gtg gag gac ttc cag gga gga aat aaa att gaa gtt Glu Trp Arg Ser Val Glu Asp Phe Gln Gly Gly Asn Lys Ile Glu Val 485	490	495	1665
aat aaa aat caa ttt gct cta att gaa gga aaa aac aaa act gta agt Asn Lys Asn Gln Phe Ala Leu Ile Glu Gly Lys Asn Lys Thr Val Ser 500	505	510	515
acc ctt gtt atc caa gcg gca aat gtg tca gct ttg tac aaa tgt gaa Thr Leu Val Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr Lys Cys Glu 520	525	530	1761
gcg gtc aac aaa gtc ggg aga gga gag agg gtg atc tcc ttc cac gtg Ala Val Asn Lys Val Gly Arg Gly Glu Arg Val Ile Ser Phe His Val 535	540	545	1809
acc agg ggt cct gaa att act ttg caa cct gac atg cag ccc act gag Thr Arg Gly Pro Glu Ile Thr Leu Gln Pro Asp Met Gln Pro Thr Glu 550	555	560	1857
cag gag agc gtg tct ttg tgg tgc act gca gac aga tct acg ttt gag Gln Glu Ser Val Ser Leu Trp Cys Thr Ala Asp Arg Ser Thr Phe Glu 565	570	575	1905
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gga gag ttg ccc aca cct gtt tgc aag aac ttg gat act ctt tgg aaa Gly Glu Leu Pro Thr Pro Val Cys Lys Asn Leu Asp Thr Leu Trp Lys 600	605	610	2001
ttg aat gcc acc atg ttc tct aat agc aca aat gac att ttg atc atg Leu Asn Ala Thr Met Phe Ser Asn Ser Thr Asn Asp Ile Leu Ile Met 615	620	625	2049
gag ctt aag aat gca tcc ttg cag gac caa gga gac tat gtc tgc ctt Glu Leu Lys Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr Val Cys Leu 630	635	640	2097
gct caa gac agg aag acc aag aaa aga cat tgc gtg gtc agg cag ctc Ala Gln Asp Arg Lys Thr Lys Lys Arg His Cys Val Val Arg Gln Leu 645	650	655	2145
aca gtc cta gag cgt gtg gca ccc acg atc aca gga aac ctg gag aat Thr Val Leu Glu Arg Val Ala Pro Thr Ile Thr Gly Asn Leu Glu Asn 660	665	670	2193
cag acg aca agt att ggg gaa agc atc gaa gtc tca tgc acg gca tct Gln Thr Thr Ser Ile Gly Glu Ser Ile Glu Val Ser Cys Thr Ala Ser 680	685	690	2241

ggg aat ccc cct cca cag atc atg tgg ttt aaa gat aat gag acc ctt Gly Asn Pro Pro Pro Gln Ile Met Trp Phe Lys Asp Asn Glu Thr Leu 695 700 705	2289
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ctt ctt ttg cca att cca cta att gtt tgg gtg aag aga aag gaa gta Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg Lys Glu Val 775 780 785	2529
cag aaa aca tgc aga aag cac aga aag gaa aac caa ggt tct cat gaa Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly Ser His Glu 790 795 800	2577
tct cca acc tta aat cct gaa aca gtg gca ata aat tta tct gat gtt Ser Pro Thr Leu Asn Pro Glu Thr Val Ala Ile Asn Leu Ser Asp Val 805 810 815	2625
gac ttg agt aaa tat atc acc act att gct gga gtc atg aca cta agt Asp Leu Ser Lys Tyr Ile Thr Thr Ile Ala Gly Val Met Thr Leu Ser 820 825 830 835	2673
caa gtt aaa ggc ttt gtt cga aag aat ggt gtc aat gaa gcc aaa ata Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu Ala Lys Ile 840 845 850	2721
gat gag atc aag aat gac aat gtc caa gac aca gca gaa cag aaa gtt Asp Glu Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu Gln Lys Val 855 860 865	2769
caa ctg ctt cgt aat tgg cat caa ctt cat gga aag aaa gaa gcg tat Gln Leu Leu Arg Asn Trp His Gln Leu His Gly Lys Lys Glu Ala Tyr 870 875 880	2817
gac aca ttg att aaa gat ctc aaa aaa gcc aat ctt tgt act ctt gca Asp Thr Leu Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys Thr Leu Ala 885 890 895	2865
ggg aaa att cag act atc atc ctc aag gac att act agt gac tca gaa Gly Lys Ile Gln Thr Ile Ile Leu Lys Asp Ile Thr Ser Asp Ser Glu 900 905 910 915	2913

aat tca aac ttc aga aat gaa atc caa agc ttg gtc tag agtgaaaaac 2962
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920 925

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<210> 10
<211> 927
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Chimeric protein
containing the extracellular domain of Flk-1 fused
in-frame to the transmembrane and cytoplasmic domains
of Fas

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 Thr Arg Ala Ala Ser Val Gly Leu Pro Ser Val Ser Leu Asp Leu Pro
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 35 40 45
 Leu Gln Ile Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro
 50 55 60
 Asn Asn Gln Ser Gly Ser Glu Gln Arg Val Glu Val Thr Glu Cys Ser
 65 70 75 80
 Asp Gly Leu Phe Cys Lys Thr Leu Thr Ile Pro Lys Val Ile Gly Asn
 85 90 95
 Asp Thr Gly Ala Tyr Lys Cys Phe Tyr Arg Glu Thr Asp Leu Ala Ser
 100 105 110
 Val Ile Tyr Val Tyr Val Gln Asp Tyr Arg Ser Pro Phe Ile Ala Ser
 115 120 125
 Val Ser Asp Gln His Gly Val Val Tyr Ile Thr Glu Asn Lys Asn Lys
 130 135 140
 Thr Val Val Ile Pro Cys Leu Gly Ser Ile Ser Asn Leu Asn Val Ser
 145 150 155 160
 Leu Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg
 165 170 175
 Ile Ser Trp Asp Ser Lys Lys Gly Phe Thr Ile Pro Ser Tyr Met Ile
 180 185 190
 Ser Tyr Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp Glu Ser
 195 200 205
 Tyr Gln Ser Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg Ile Tyr
 210 215 220
 Asp Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu
 225 230 235 240
 Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile
 245 250 255
 Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu
 260 265 270
 Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe
 275 280 285

Leu Ser Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu
 290 295 300
 Tyr Thr Cys Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr
 305 310 315 320
 Phe Val Arg Val His Glu Lys Pro Phe Val Ala Phe Gly Ser Gly Met
 325 330 335
 Glu Ser Leu Val Glu Ala Thr Val Gly Glu Arg Val Arg Ile Pro Ala
 340 345 350
 Lys Tyr Leu Gly Tyr Pro Pro Glu Ile Lys Trp Tyr Lys Asn Gly
 355 360 365
 Ile Pro Leu Glu Ser Asn His Thr Ile Lys Ala Gly His Val Leu Thr
 370 375 380
 Ile Met Glu Val Ser Glu Arg Asp Thr Gly Asn Tyr Thr Val Ile Leu
 385 390 395 400
 Thr Asn Pro Ile Ser Lys Glu Lys Gln Ser His Val Val Ser Leu Val
 405 410 415
 Val Tyr Val Pro Pro Gln Ile Gly Glu Lys Ser Leu Ile Ser Pro Val
 420 425 430
 Asp Ser Tyr Gln Tyr Gly Thr Thr Gln Thr Leu Thr Cys Thr Val Tyr
 435 440 445
 Ala Ile Pro Pro Pro His His Ile His Trp Tyr Trp Gln Leu Glu Glu
 450 455 460
 Glu Cys Ala Asn Glu Pro Ser Gln Ala Val Ser Val Thr Asn Pro Tyr
 465 470 475 480
 Pro Cys Glu Glu Trp Arg Ser Val Glu Asp Phe Gln Gly Gly Asn Lys
 485 490 495
 Ile Glu Val Asn Lys Asn Gln Phe Ala Leu Ile Glu Gly Lys Asn Lys
 500 505 510
 Thr Val Ser Thr Leu Val Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr
 515 520 525
 Lys Cys Glu Ala Val Asn Lys Val Gly Arg Gly Glu Arg Val Ile Ser
 530 535 540
 Phe His Val Thr Arg Gly Pro Glu Ile Thr Leu Gln Pro Asp Met Gln
 545 550 555 560
 Pro Thr Glu Gln Glu Ser Val Ser Leu Trp Cys Thr Ala Asp Arg Ser
 565 570 575
 Thr Phe Glu Asn Leu Thr Trp Tyr Lys Leu Gly Pro Gln Pro Leu Pro
 580 585 590
 Ile His Val Gly Glu Leu Pro Thr Pro Val Cys Lys Asn Leu Asp Thr
 595 600 605
 Leu Trp Lys Leu Asn Ala Thr Met Phe Ser Asn Ser Thr Asn Asp Ile
 610 615 620
 Leu Ile Met Glu Leu Lys Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr
 625 630 635 640
 Val Cys Leu Ala Gln Asp Arg Lys Thr Lys Lys Arg His Cys Val Val
 645 650 655
 Arg Gln Leu Thr Val Leu Glu Arg Val Ala Pro Thr Ile Thr Gly Asn
 660 665 670
 Leu Glu Asn Gln Thr Thr Ser Ile Gly Glu Ser Ile Glu Val Ser Cys
 675 680 685
 Thr Ala Ser Gly Asn Pro Pro Pro Gln Ile Met Trp Phe Lys Asp Asn
 690 695 700
 Glu Thr Leu Val Glu Asp Ser Gly Ile Val Leu Lys Asp Gly Asn Arg
 705 710 715 720
 Asn Leu Thr Ile Arg Arg Val Arg Lys Glu Asp Glu Gly Leu Tyr Thr
 725 730 735

Cys Gln Ala Cys Ser Val Leu Gly Cys Ala Lys Val Glu Ala Phe Phe
 740 745 750
 Ile Ile Glu Gly Ala Gln Glu Lys Gly Ser Arg Ser Asn Leu Gly Trp
 755 760 765
 Leu Cys Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg
 770 775 780
 Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly
 785 790 795 800
 Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val Ala Ile Asn Leu
 805 810 815
 Ser Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Ile Ala Gly Val Met
 820 825 830
 Thr Leu Ser Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu
 835 840 845
 Ala Lys Ile Asp Glu Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu
 850 855 860
 Gln Lys Val Gln Leu Leu Arg Asn Trp His Gln Leu His Gly Lys Lys
 865 870 875 880
 Glu Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys
 885 890 895
 Thr Leu Ala Gly Lys Ile Gln Thr Ile Ile Leu Lys Asp Ile Thr Ser
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 Asp Ser Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln Ser Leu Val
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 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: Primer

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27

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30

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